

US-09-613-508b-2 (1-303) x US-09-227-721-31 (1-1440)
 QY 176 GUAUAPROLYLAUPEAPHEALIGUALACYS 186
 DB 1042 GMAAACTTAACTCTTTTCATCCAGCCCTGC 1074

RESULT 10
 US-08-665-220-1
 Sequence 1, Application US/08665220
 Patent No. 5786173
 GENERAL INFORMATION:
 APPLICANT: Alimenti, Emd S.
 APPLICANT: Fernandez-Alimenti, Teresa
 APPLICANT: Litwack, Gerald
 APPLICANT: Armstrong, Robert
 APPLICANT: Litwack, Gerald
 TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
 TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: 08/665/220
 APPLICATION NUMBER: 08/665/220
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9001
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/618 408
 FILING DATE: 04-11-1999
 NAME: Christlanger, William T.
 REGISTRATION NUMBER: 44,614
 REFERENCE/DOCKET NUMBER: 480140.124C3
 TELEPHONE/DOCKET NUMBER: 106/422-4900
 TELEFAX: (206) 689-6031
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1700 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 148..1584
 OTHER INFORMATION: /note= "Mch4"

Alignment Scores:
 Pred. No.: 0.0671 Length: 1700
 Score: 11.00 Matches: 11
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 3.63% Indels: 0
 DB: Gaps: 0

US-09-613-508b-2 (1-303) x US-08-665-220-1 (1-1700)
 QY 176 GUAUAPROLYLAUPEAPHEALIGUALACYS 186
 DB 1189 GMAAACTTAACTCTTTTCATCCAGCCCTGC 1221

US-09-291-692-1
 QY 176 GUAUAPROLYLAUPEAPHEALIGUALACYS 186
 DB 1189 GMAAACTTAACTCTTTTCATCCAGCCCTGC 1221

RESULT 11
 US-09-291-692-1
 Sequence 1, Application US/09291692
 Patent No. 6586235
 GENERAL INFORMATION:
 APPLICANT: Alimenti, Emd S.
 APPLICANT: Fernandez-Alimenti, Teresa
 APPLICANT: Litwack, Gerald
 APPLICANT: Armstrong, Robert
 APPLICANT: Tomaseill, Kevin
 TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
 TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSER: SEED AND BERRY
 STREET: 6100 Columbia Center, 701 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: Use
 ZIP: 98104

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 09/291/692
 APPLICATION NUMBER: US/09/291,692
 FILING DATE: 04-11-1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/291,692
 NAME: Christlanger, William T.
 REGISTRATION NUMBER: 44,614
 REFERENCE/DOCKET NUMBER: 480140.124C3
 TELEPHONE/DOCKET NUMBER: 106/422-4900
 TELEFAX: (206) 689-6031
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1700 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 148..1584
 OTHER INFORMATION: /note= "Mch4"

Alignment Scores:
 Pred. No.: 0.0671 Length: 1700
 Score: 11.00 Matches: 11
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 3.63% Indels: 0
 DB: Gaps: 0

US-09-613-508b-2 (1-303) x US-09-291-692-1 (1-1700)
 QY 176 GUAUAPROLYLAUPEAPHEALIGUALACYS 186
 DB 1189 GMAAACTTAACTCTTTTCATCCAGCCCTGC 1221

RESULT 12
 US-09-982-8344-1
 Sequence 1, Application US/099828344
 Patent No. 6586235
 GENERAL INFORMATION:
 APPLICANT: Bowman, Michael
 TITLE OF INVENTION: NOVEL PROTEASE

NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 COUNTRY: USA
 STATE: Massachusetts
 ZIP: 02140

COMPUTER READABLE FORM:
 MEDIA TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US 09/962,834A
 FILING DATE: 25-SEP-2001
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/075,123
 FILING DATE: 09/07/95

ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott R.
 REGISTRATION NUMBER: 2,724
 ADDRESS: 10000 Wilshire Blvd., Suite 1000
 TELEPHONE: (617) 498-8224

TELEPHONE: (617) 498-8224
 TELEPHONE: (617) 498-8224
 INFORMATION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1704 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..163
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-962-834A-1

Alignment Scores:
 Score No.: 0.0672 Length: 11704
 11.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 DB: 4 638 Gaps: 0

US-09-613-508b-2 (1-303) x US-09-962-834A-1 (1-1704)
 QY 176 GluYpProlvslslempPheP11gclnlnA1Cy6 186
 DB 1281 GAAAACTTAACCTTTTCATCCAGCCCTCC 1323

RESULT 13
 US-08-724-378D-1
 Sequence 1, Application US/08724378D
 Patent No. 6512104
 GENBANK INFORMATION:
 APPLICANT: SHAO-CHIH
 APPLICANT: FLETCHER, FREDERICK A.
 TITLE OF INVENTION: INTERLEUKIN-1-BETA CONVERTING ENZYME LIKE CYSTEINE
 FILE REFERENCE: 06843-0019-0000
 CURRENT APPLICATION NUMBER: US/08/724,378D
 CURRENT FILING DATE: 1996-10-01
 SOFTWARE: SEQ ID NO: 1
 DB: 2 1
 LENGTH: 2152
 TPEL: DNA
 ORIGIN: Homo sapiens

FEATURE:
 NAME/KEY: CDS
 LOCATION: (170) ..(1336)
 US-08-724-378D-1

Alignment Scores:
 Pred. No.: 0.0834 Length: 2152
 Score: 11.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 DB: 4 638 Gaps: 0

US-09-613-508b-2 (1-303) x US-08-724-378D-1 (1-2152)
 QY 176 GluYpProlvslslempPheP11gclnlnA1Cy6 186
 DB 941 GAAAACTTAACCTTTTCATCCAGCCCTCC 973

RESULT 14
 US-08-618-408B-1
 Sequence 1, Application US/08618408B
 Patent No. 6518183
 GENBANK INFORMATION:
 APPLICANT: Alimonti, Rand S.
 APPLICANT: Fernandez-Alimonti, Teresa
 APPLICANT: Llewellyn, Gerald
 APPLICANT: Llewellyn, Gerald
 APPLICANT: Tomasek, Kevin
 TITLE OF INVENTION: Wch4 and Mch4, No. 586181se1 Apoptotic
 TITLE OF INVENTION: Procress, Nucleic Acids Encoding and Methods of Use
 ADDRESS: 4370 La Jolla Village Drive, Suite 700
 STREET: San Diego
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIA TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US 08/618,408B
 FILING DATE: 19-SEP-1996
 CLASSIFICATION: 425
 ATTORNEY/AGENT INFORMATION:
 NAME/KEY: A
 REGISTRATION NUMBER: 7311, 815
 REFERENCE/DOCKET NUMBER: P-ID 1957
 TELEPHONE: (619) 3584001
 TELEPHONE: (619) 3584001
 LENGTH: 3935 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1554
 FEATURE: 546 .. 1554
 NAME/KEY: misc feature
 LOCATION: 1..1535
 DB: 1
 LENGTH: 11
 US-08-618-408B-1

Alignment Scores:
 Score No.: 0.112 Length: 3535
 11.00 Matches: 11

[illegible]

QY 261 Gnlaprocysallelsertleuthrysglueutyphenyths 277
DB 1004 CMAATCCATGATATGCTTCATCTCCACCAAGACCTGATTTTATTCAC 1054

RESULT 5
US-08-462-969B-3
Sequence 3: Application US/08462969B
Accession: 609313
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 beta Converting Enzyme
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION IN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08462,969B
FILING DATE: 05-JUN-1995
PUBLICATION DATE: 514
PRIORITY DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: Andreev 373
REFERENCE/DOCKET NUMBER: PF140P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-3504
FAX: 301-309-3504
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1159 base pairs
SYNTHESIS METHOD: Synthetic acid
STRANDS: 1
TOPOLOGY: Linear

US-08-462-969B-3
MOLECULE TYPE: DNA (genomic)

Alignment Scores:
Pred. No.: 1,97e-280 Length: 1159
Score: 277.00 Matches: 277
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Gaps: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-613-508B-4 (1-277) x US-08-462-969B-3 (1-1159)

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QY 21 Ttshselysgclubnsertlalsesryysertlelyabamlencluproyalle 40
DB 283 ATGATCCACCAAGACCTGATGATCATTAATCATTAATTCATGACCAAGATC 342

QY 41 TTPProdlwsgclubnsertlalsesryysertlelyabamlencluproyalle 60
DB 343 TACCTCCACCAAGACCTGATGATCATTAATCATTAATTCATGACCAAGATC 402

QY 61 McTtshseryysertlalsesryysertlelyabamlencluproyalle 80

DB 403 ATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 462
QY 81 Ttshseryysertlalsesryysertlelyabamlencluproyalle 100
DB 463 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522

QY 101 ATGAPVAlserlysgclubnsertlalsesryysertlelyabamlencluproyalle 120
DB 523 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 582

QY 121 HsaglYglubnsglye11pshelythramlypProvalasleuylslytr 140
DB 583 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 642

QY 141 AsnpPshseryysertlalsesryysertlelyabamlencluproyalle 160
DB 643 ACTTTTCAGAGGAGATCTGTGTGAGAGTCAACTGAGAAACCCCAACTTTT 702

QY 161 Gnlalacyseryysertlalsesryysertlelyabamlencluproyalle 180
DB 703 CAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 762

QY 181 AsnpPshseryysertlalsesryysertlelyabamlencluproyalle 200
DB 763 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 822

QY 201 Prccllythrysgclubnsertlalsesryysertlelyabamlencluproyalle 220
DB 823 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 882

QY 221 Almetlethrysgclubnsertlalsesryysertlelyabamlencluproyalle 240
DB 883 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 942

QY 241 ATGylvaltthrysgclubnsertlalsesryysertlelyabamlencluproyalle 260
DB 943 CAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002

QY 261 Gnlaprocysallelsertleuthrysglueutyphenyths 277
DB 1003 CMAATCCATGATATGCTTCATCTCCACCAAGACCTGATTTTATTCAC 1053

RESULT 6
US-09-124-934A-3
Sequence 3: Application US/09124934A
Accession: 6495519
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 beta Converting Enzyme Like Apoptosis Protease
FILE REFERENCE: PFI40C1
CURRENT FILING DATE: 1994-11-01
CURRENT APPLICATION NUMBER: US/09124,934A
INVENTOR: PFI40C1
PUBLICATION DATE: 1994-11-01
PRIORITY DATE: 1994-11-01
SEQUENCE CHARACTERISTICS:
LENGTH: 1159
SYNTHESIS METHOD: Synthetic acid
STRANDS: 1
TOPOLOGY: Linear

US-09-124-934A-3
MOLECULE TYPE: DNA (genomic)

Alignment Scores:
Pred. No.: 1,97e-280 Length: 1159
Score: 277.00 Matches: 277
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Gaps: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-613-508B-4 (1-277) x US-09-124-934A-3 (1-1159)

QY 1 Mcglubntgclubnsertlalsesryysertlelyabamlencluproyalle 20
DB 223 ATGGAGACACCTGAAATCTGATGATCATTAATCATTAATTCATGACCAAGATC 282


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Db 920 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 979
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Db 980 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 1039
Oy 129 GATTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
Db 1040 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 1099
Oy 149 ArgSerLeuThiGlyValProValLeuPheLeuIleGlnValGlyValGlnValGlnVal 168
Db 1100 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 1159
Oy 169 ArgSerLeuThiGlyValProValLeuPheLeuIleGlnValGlyValGlnValGlnVal 188
Db 1160 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 1219
Oy 189 ValGlnValLeuPheLeuIleGlnValGlyValGlnValGlnValGlnValGlnValGln 208
Db 1220 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 1279
Oy 209 SerTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 221
Db 1280 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 1318

RESUME 11
US-09-561-756-10
/ Sequence 10, Application US/09561756
/ Patent No. 6379226
/ GENERAL INFORMATION: Read S
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
/ FILE REFERENCE: 480140.431
/ CURRENT APPLICATION NUMBER: US/09/561.756
/ PRIORITY DATE: 09/22/721
/ PRIOR FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: SeqScribe for Windows Version 3.0
/ SEQ ID NO: 10
/ LENGTH: 835
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ NAME/KEY: misc feature
/ LOCATION: (1) -- (835)
/ OTHER INFORMATION: n = A, T, C or G
US-09-561-756-10

Alignment Scores:
Pred. No.: 1,536-188 Length: 835
Score: 189.200 Matches: 0
Percent Similarity: 99.284 Mismatches: 0
Best Local Similarity: 99.284 Indels: 2
Query Match: 68,234 Gaps: 0

US-09-613-508b-4 (1-277) x US-09-561-756-10 (1-835)
Oy 1 MetGluAsnThrGlnAsnValAspSerValSerTLeuValLeuGluProGlyIle 20
Db 1 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 60
Oy 211 MetGluAsnThrGlnAsnValAspSerValSerTLeuValLeuGluProGlyIle 40
Db 61 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 120
Oy 41 TyrProIleuValGlyValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 60
Db 121 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 180

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Oy 61 MetTserGlySerGlyValAspValLeuValLeuValLeuValLeuValLeuValLeuVal 80
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Oy 81 LeuValGlyValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 100
Db 241 TGGAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Oy 101 ArgSerValSerValGlnValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 120
Db 301 CATTGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 360
Oy 121 MetGluAsnThrGlnAsnValAspSerValSerTLeuValLeuGluProGlyIle 140
Db 361 CATTGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 420
Oy 141 AsnThrPheValGlyValAspValLeuValLeuValLeuValLeuValLeuValLeuValLeu 160
Db 421 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 480
Oy 161 GlnValGlyValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 180
Db 481 CATTGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 540
Oy 181 ArgSerValSerValGlnValLeuValLeuValLeuValLeuValLeuValLeuValLeu 200
Db 541 CATTGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 599
Oy 200 ArgGlyValTyrSerTLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 220
Db 600 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 559
Oy 220 GlnValGlyValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 240
Db 660 TCCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Oy 240 ArgGlyValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 260
Db 720 CCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
Oy 260 GlnValGlyValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 277
Db 780 AATGCTTACACCTGAGAGAAATTTGCGAATATGATGCTATGCTTTCTAAAGAGATATCC 831

RESUME 12
US-09-227-721-10
/ Sequence 10, Application US/09227721
/ Patent No. 6379950
/ GENERAL INFORMATION: Read S
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
/ FILE REFERENCE: 480140.431
/ CURRENT APPLICATION NUMBER: US/09/227.721
/ PRIORITY DATE: 09/22/721
/ PRIOR FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: SeqScribe for Windows Version 3.0
/ SEQ ID NO: 10
/ LENGTH: 835
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ NAME/KEY: misc feature
/ LOCATION: (1) -- (835)
/ OTHER INFORMATION: n = A, T, C or G
US-09-227-721-10

Alignment Scores:
Pred. No.: 1,536-188 Length: 835
Score: 189.200 Matches: 0
Percent Similarity: 99.284 Mismatches: 0
Best Local Similarity: 99.284 Indels: 2
Query Match: 68,234 Gaps: 0

```


